AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method to detect Incontinentia Pigmenti in a human comprising the steps of:

obtaining a sample from said [organism] human; and

analyzing said sample for an alteration in a nucleic acid of SEQ ID NO:1.

2. (Original) The method of Claim 1, wherein said alteration is a mutation, wherein said mutation is selected from the group consisting of a deletion, an insertion, a point mutation, a rearrangement in said sequence, and a combination thereof.

3. (Original) The method of Claim 2, wherein said point mutation is selected from the group consisting of a nonsense mutation, a frameshift mutation, a missense mutation, a splicing-related mutation, and a combination thereof.

4. (Currently Amended) The method of Claim 1, wherein said alteration is located in a regulatory ~~nucleic acid, a promoter nucleic acid~~ region, an exon, an intron, an initiator codon, a stop codon, an exon/intron junction, a 5′ untranslated region, a 3′ untranslated region ~~and~~ or a combination thereof.

5. (Original) The method of Claim 1, wherein said analyzing step comprises a method selected from the group consisting of hybridization, SSCP, heteroduplex analysis, sequencing, polymerase chain reaction, electrophoresis, and a combination thereof.

6-31. (Previously Cancelled)

32. (Currently Amended) A method to detect an alteration in a nucleic acid of SEQ ID NO:1 in [an organism] a human, comprising the steps of:

obtaining a sample from said [organism] human; and

analyzing said sample for said alteration.

33. (Original) The method of Claim 32, wherein said alteration is a mutation, wherein

said mutation is selected from the group consisting of a deletion, an insertion, point mutation, a rearrangement, and a combination thereof.

34. (Original) The method of Claim 33, wherein said point mutation is selected from the group consisting of a nonsense mutation, a frameshift mutation, a missense mutation, a splicing-related mutation, and a combination thereof.

35. (Currently Amended) The method of Claim 32, wherein said alteration is located in a regulatory ~~nucleic acid, a promoter nucleic acid~~ region, an exon, an intron, an initiator codon, a stop codon, an exon/intron junction, a 5′ untranslated region, a 3′ untranslated region ~~and~~ or a combination thereof.

36. (Original) The method of Claim 32, wherein said analyzing step comprises a method selected from the group consisting of hybridization, SSCP, heteroduplex analysis, sequencing, polymerase chain reaction, electrophoresis, and a combination thereof.

37. (Cancel)

38. (Currently Amended) The method of Claim 32, wherein said ~~organism is a~~ human is selected from the group consisting of an affected individual, a carrier individual, ~~or~~ and a noncarrier individual.

39. (Original) The method of claim 32, wherein said analyzing step further comprises a technique selected from the group consisting of PCR analysis and Southern blot analysis.

40-42. (Previously Cancelled)

43. (Original) The method of Claim 39, wherein a probe for said Southern analysis is a nucleic acid of SEQ ID NO:3, or fragments and derivatives thereof.

Claims 44-50. (Previously Cancelled)

51-53. (Cancel)